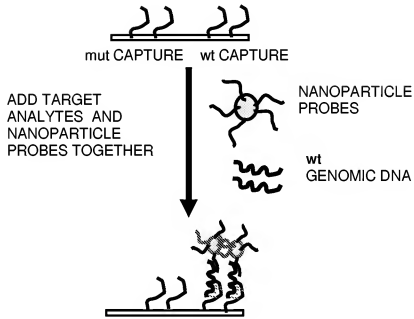
FIG. 1



SPECIFIC BINDING OF NANOPARTICLE PROBES TO wt CAPTURE PROBES VIA wt TARGET ANALYTE IN A SANDWICH FORMAT

FIG. 2

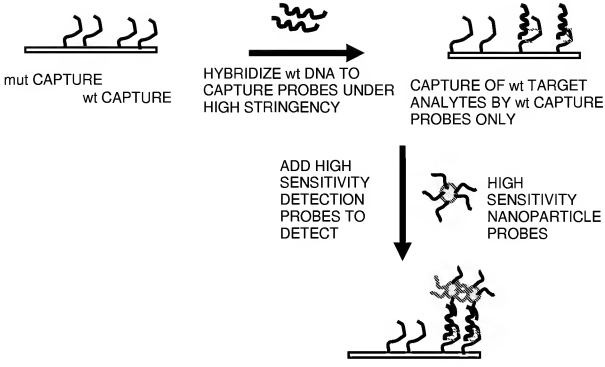

mut CAPTURE
wt CAPTURE
HYBRIDIZE wt DNA TO CAPTURE PROBES UNDER HIGH STRINGENCY
CAPTURE OF wt TARGET ANALYTES BY wt CAPTURE PROBES ONLY
ADD HIGH SENSITIVITY DETECTION PROBES TO DETECT
HIGH SENSITIVITY NANOPARTICLE PROBES

FIG. 3

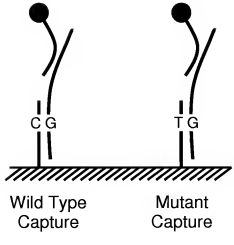

C G
T G
Wild Type Capture
Mutant Capture

FIG. 4A

10ug OF NORMAL HUMAN GENOMIC DNA

Mut

WT

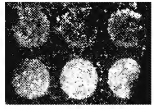


FIG. 4B

10UG OF SALMON SPERM DNA

Mut

WT

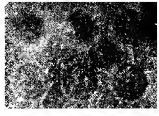


FIG. 4C

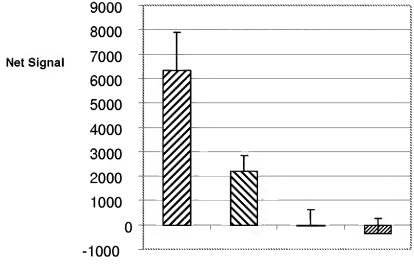


FIG. 5

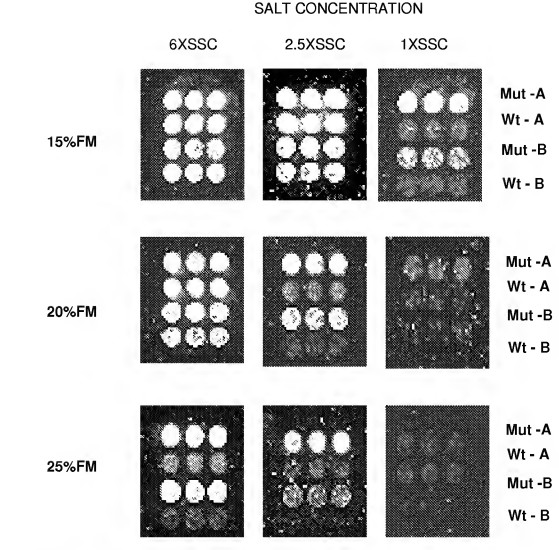

SALT CONCENTRATION
6XSSC
2.5XSSC
1XSSC
15%FM
20%FM
25%FM
Mut -A
Wt - A
Mut -B
Wt - B
Mut -A
Wt - A
Mut -B
Wt - B
Mut -A
Wt - A
Mut -B
Wt - B
FORMAMIDE
CONCENTRATION

FIG. 6A

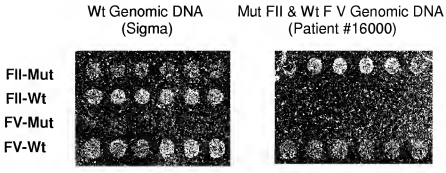


FIG. 6B

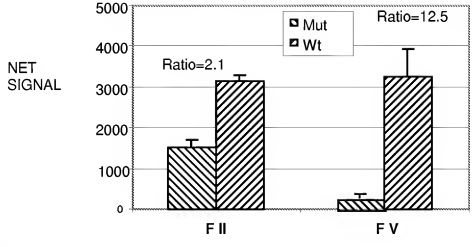


FIG. 6C

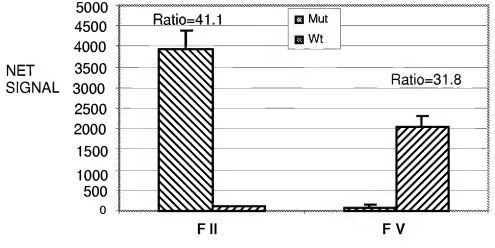


FIG. 7A

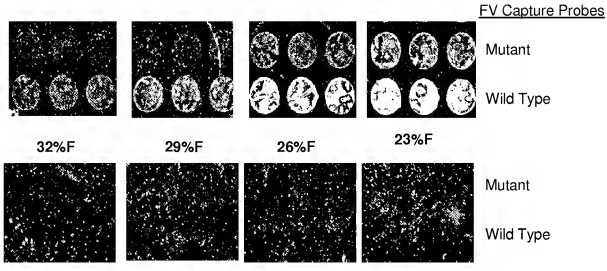

FV Capture Probes
Mutant
Wild Type
32%F
29%F
26%F
23%F
Mutant
Wild Type

FIG. 7B

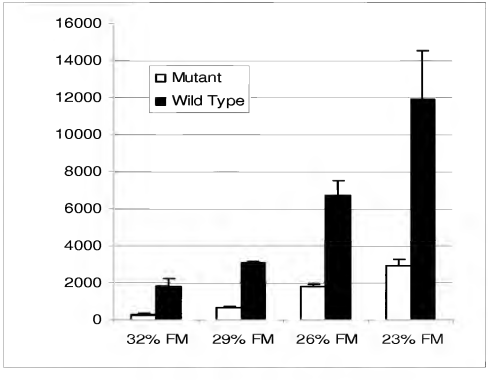

16000
14000
12000
10000
8000
6000
4000
2000
0
Mutant
Wild Type
32% FM
29% FM
26% FM
23% FM

FIG. 8

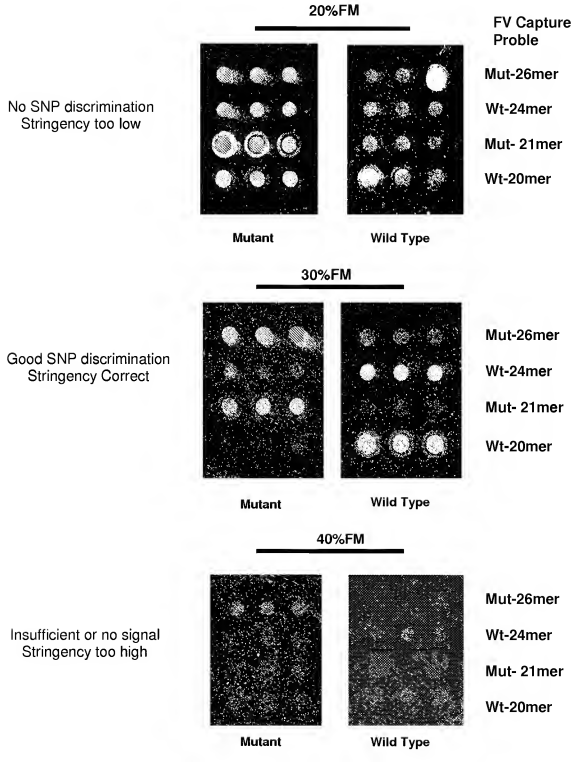

20%FM
FV Capture Proble
Mut-26mer
Wt-24mer
Mut- 21mer
Wt-20mer
No SNP discrimination
Stringency too low
Mutant
Wild Type
30%FM
Mut-26mer
Wt-24mer
Mut- 21mer
Wt-20mer
Good SNP discrimination
Stringency Correct
Mutant
Wild Type
40%FM
Mut-26mer
Wt-24mer
Mut- 21mer
Wt-20mer
Insufficient or no signal
Stringency too high
Mutant
Wild Type

FIG. 9A

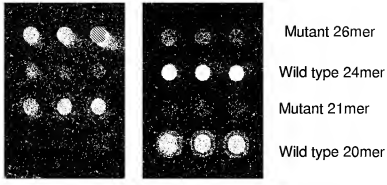
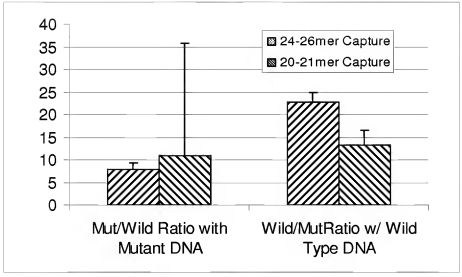
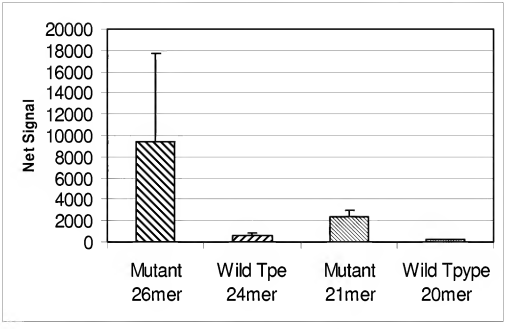


FIG. 9B



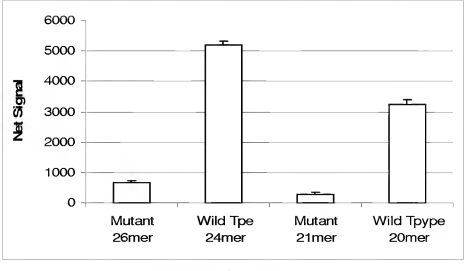
RATIO OF SIGNAL INTENSITIES

FIG. 9C



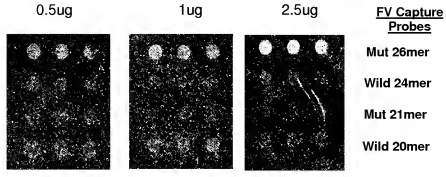
HYBRIDIZATION WITH MUTANT GENOMIC DNA

FIG. 9D



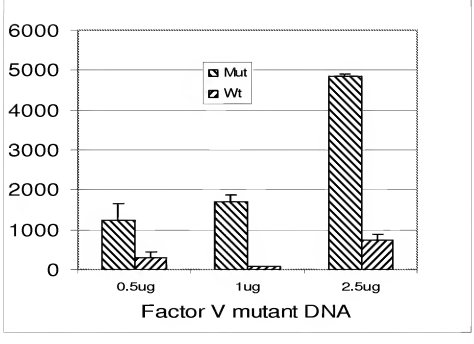
HYBRIDIZATION WITH
WILD TYPE GENOMIC DNA

FIG. 10A



IMAGES OF FAC.V ARRAY HYBRIDIZED WITH MUTANT GENOMIC DNA.

FIG. 10B



SIGNAL INTENSITIES FOR MUTANT (26MER) AND WILD TYPE (24MER) CAPTURE PROBES

FIG. 11A

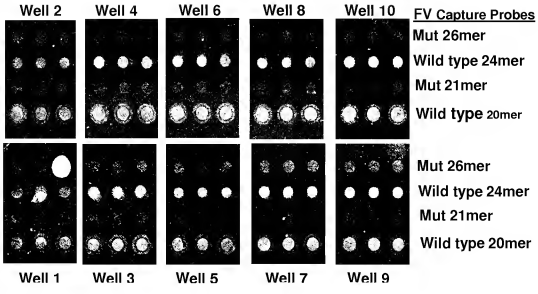


FIG. 11B

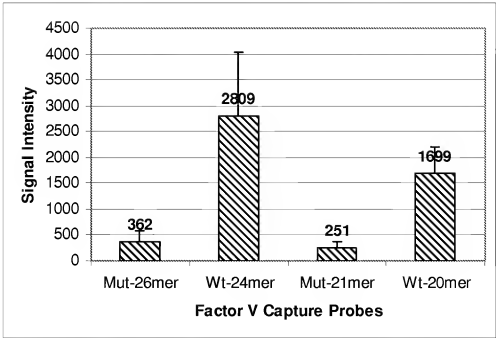


FIG. 12A

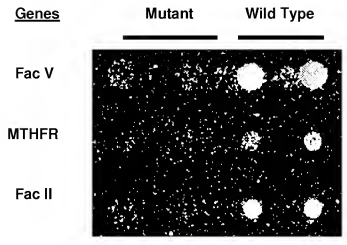


FIG. 12B

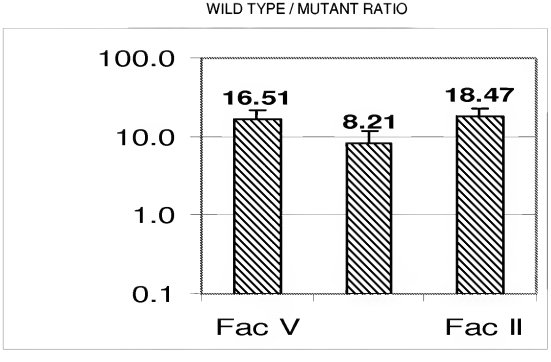


FIG. 13A

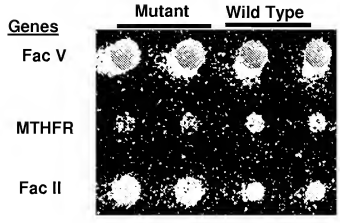


FIG. 13B

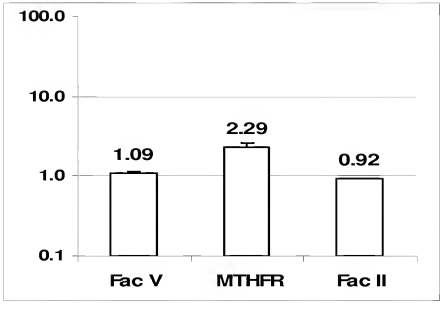


FIG. 14A

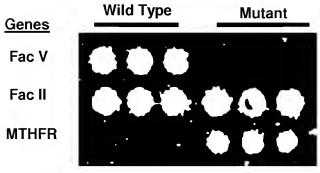


FIG. 14B

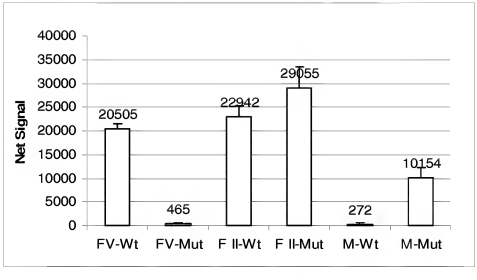


FIG. 14C

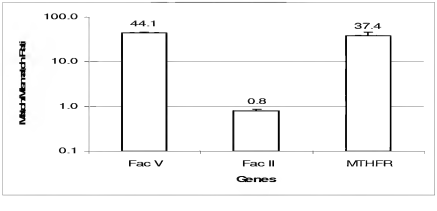


FIG. 15A

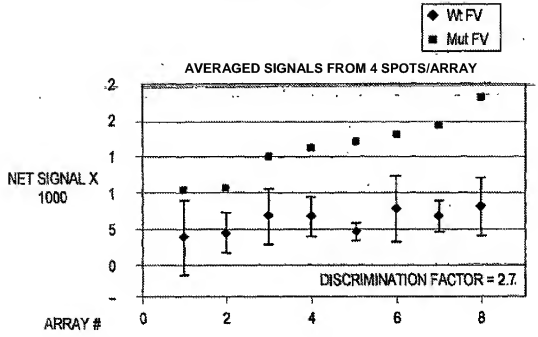


FIG. 15B

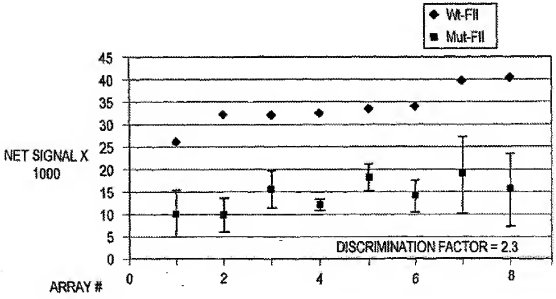


FIG. 15C

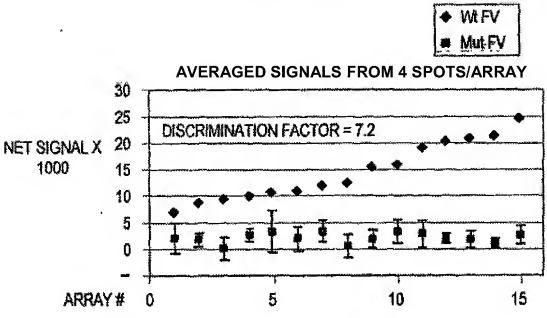


FIG. 15D

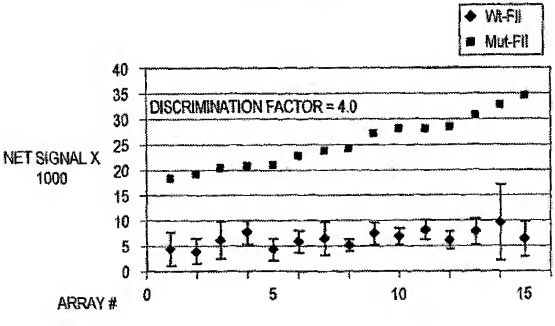


FIG. 16A

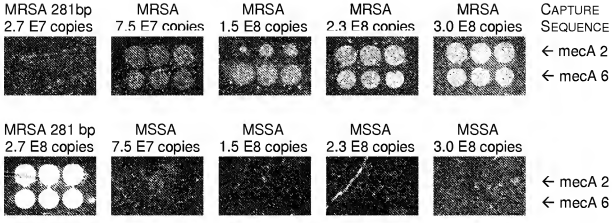


FIG. 16B

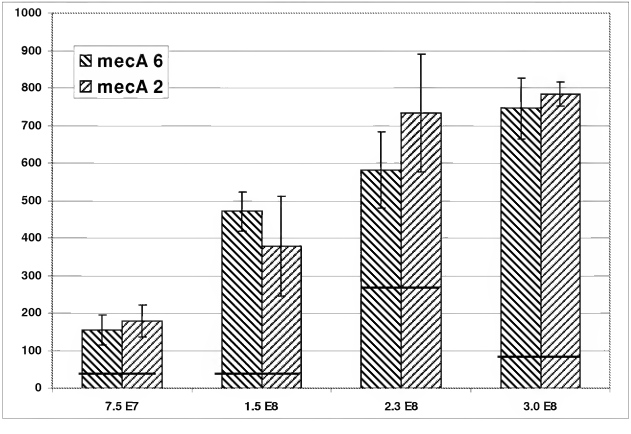


FIG. 17A

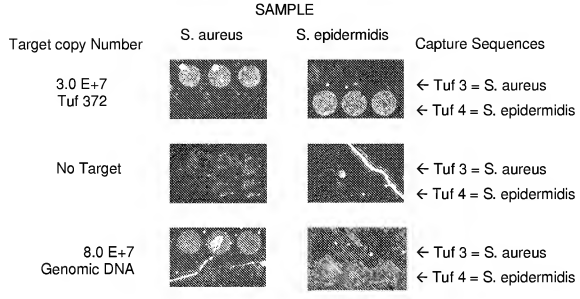


FIG. 17B

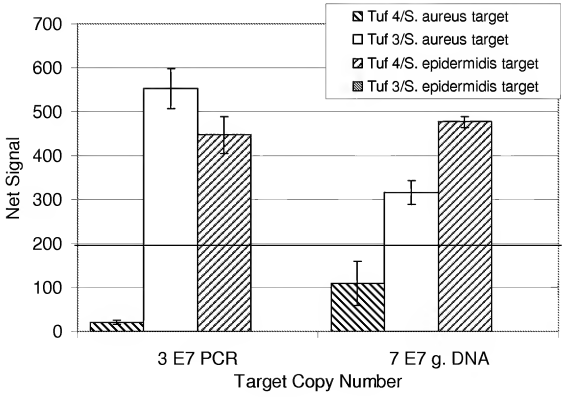


FIG. 17C

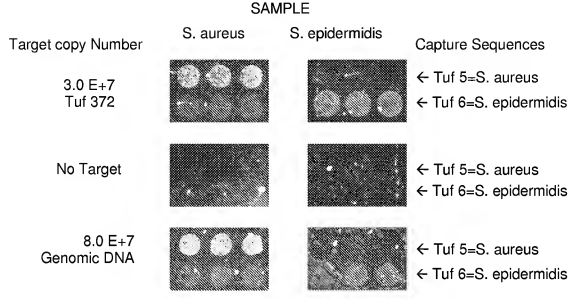


FIG. 17D

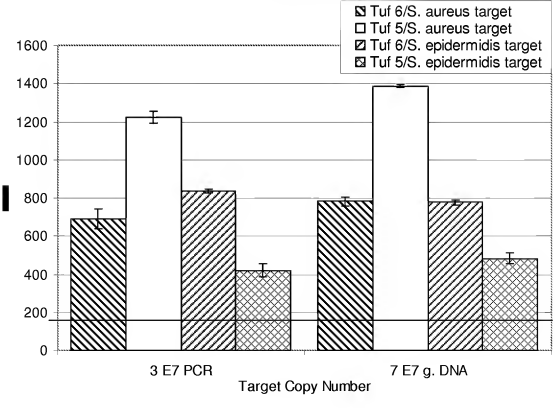


FIG. 18

Name	Template Species	gene	Length	Sequence 5'→3'
mecA 281	*S. aureus*	*mecA*	281	(coding strand)

ATCCACCCTCAAACAGGTGAATTATTAGCATTGTAAGCACACCTTCATATGACGTCTATCCATTTATGTATGGCAT
GAGTAACGAAGAATATAATAAATTAACCGAAGATAAAAAAGAACCTCTGCTCAAGTCAATCCAGATTACAACTTCA
CCAGGTTCAACTCAAAAAATATTAACAGCAATGATTGGGTTAAATAACAAAACATTAGACGATAAAACAAGTTATA
AAATCGATGGTAAAGGTTGGCAAAAAGATAAATCTTGGGGTGGTTACAACGT

Coa	*S. aureus*	coagulase	480

CGAGACCAAGATTCAACAAGCCAAGTGAAACAAATGCATACAACGTAACGACAAATCAAGATGGCACAGTATCATA
CGGAGCTCGCCCAACACAAAACAAGCCAAGTGAAAAAACGCATATAACGTAACAACACATGCAAATGGTCAAGTAT
CATACGGTGCTCGCCCAACACAAACAAGCCAAGCAAAACAAATGCATACAACGTAACAACACATGCAAATGGTCAA
GTATCATATGGCGCTCGCCCGACACAAAAAAAGCCAAGCAAAACAAATGCATATAACGTAACAACACATGCAAATG
GTCAAGTATCATACGGAGCTCGCCCGACATACAAGAAGCCAAGCGAAACAAATGCATACAACGTAACAACACATGC
AAATGGTCAAGTATCATATGGCGCTCGCCCGACACAAAAAAAGCCAAGCGAAACAAACGCATATAACGTAACAACA
CATGCAGATGGTACTGCGACAT

Tuf 142	*S. aureus*	*Tuf*	142

GTGGTCAAGTATTAGCTGCTCCTGGTTCAATTACACCACATACTGAATTCAAAGCAGAAGTATACGTATTATCAAA
AGACGAAGGTGGACGTCACACTCCATTCTTCTCARACTATCGTCCACAATTCTATTTCCGTACTAC

Tuf 372	*S. aureus*	*Tuf*	372

TGATGCCRGTTGAGGACGTATTCTCAATCACTGGTCGTGGTACTGTTGCTACAGGCCGTGTTGAACGTGGTCAAAT
CAAAGTTGGTGAAGAAGTTGAAATCATCGGTTTACATGACACATCTAAAACAACTGTTACAGGTGTTGAAATGTTC
CGTAAATTATTAGACTACGCTGAAGCTGGTGACAACATTGGTGCATTATTACGTGGTGTTGCTCGTGAAGACGTAC
AACGTGGTCAAGTATTAGCTGCTCCTGGTTCAATTACACCACATACTGAATTCAAAGCAGAAGTATACGTATTATC
AAAAGACGAAGGTGGACGTCACACTCCATTCTTCTCARACTATCGTCCACAATTCTATTTCCGTACTAC

Tuf 372	*S. epidermidis*	*Tuf*	372

TGATGCCAGTTGAGGACGTATTCTCAATCACTGGTCGTGGTACTGTTGCTACAGGCCGTGTTGAACGTGGTCAAAT
CAAAGTTGGTGAAGAAGTTGAAATCATCGGTATGCACGAAACTTCTAAAACAACTGTTACTGGTGTAGAAATGTTC
CGTAAATTATTAGACTACGCTGAAGCTGGTGACAACATCGGTGCTTTATTACGTGGTGTTGCACGTGAAGACGTAC
AACGTGGTCAAGTATTAGCTGCTCCTGGTTCTATTACACCACACACAAAATTCAAAGCTGAAGTATACGTATTATC
TAAAGATGAAGGTGGACGTCACACTCCATTCTTCACTAACTATCGCCCACAATTCTATTTCCGTACTAC

Tuf 372	*S. saprophyticus*	*Tuf*	372

TGATGCCAGTTGAGGACGTATTCTCAATCACTGGTCGTGGTACTGTTGCTACAGGCCGTGTTGAACGTGGTCAAAT
CAAAGTCGGTGAAGAAATCGAAATCATCGGTATGCAAGAAGAATCAAGCAAAACAACTGTTACTGGTGTAGAAATG
TTCCGTAAATTATTAGACTACGCTGAAGCTGGTGACAACATTGGTGCATTATTACGTGGTGTTTCACGTGATGATG
TACAACGTGGTCAAGTTTTAGCTGCTCCTGGTACTATCACACCACATACAAAATTCAAAGCGGATGTTTACGTTTT
ATCTAAAGATGAAGGTGGTCGTCATACGCCATTCTTCACTAACTACCGCCCACAATTCTATTTCCGTACTACTGAC

16S	*Staphylococcus*	*16S*	451

CGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAGAACAAACGTGTAAGTAACTGTGC
ACGTCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGC
GTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCG
TGGAGGGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGC
AGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGA
TCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCC

FIG. 19A

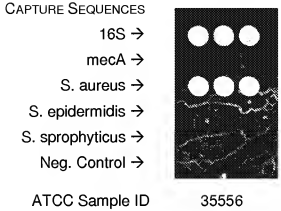


FIG. 19B

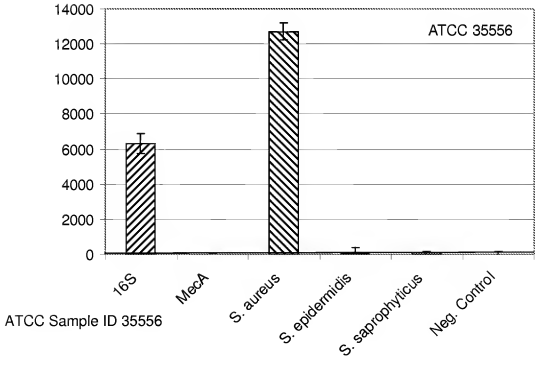


FIG. 19C

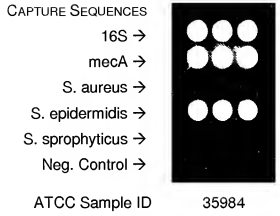


FIG. 19D

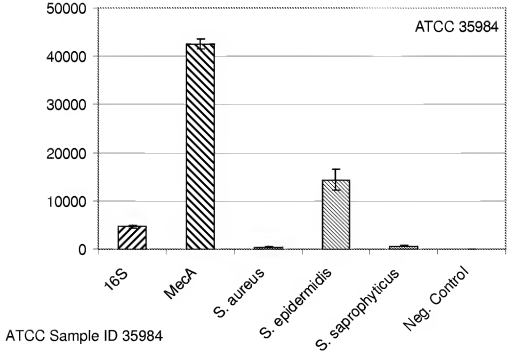


FIG. 19E

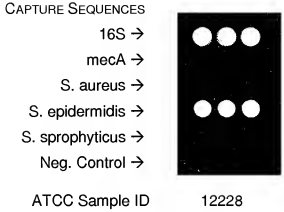


FIG. 19F

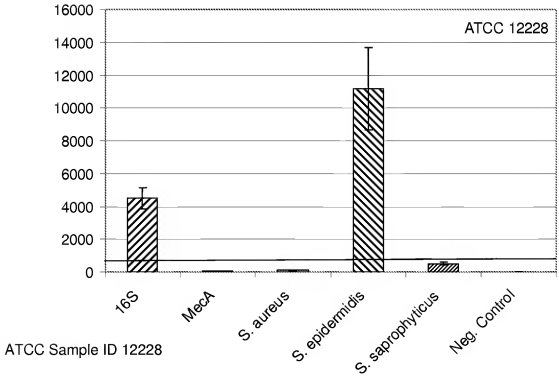


FIG. 19G

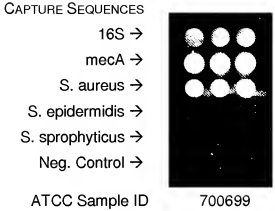


FIG. 19H

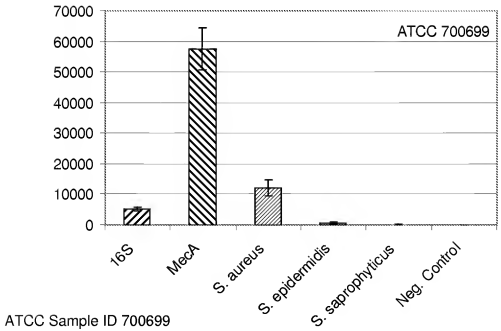


FIG. 19I

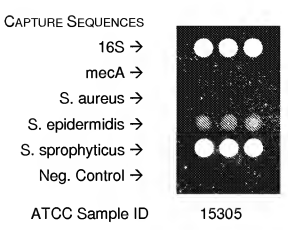
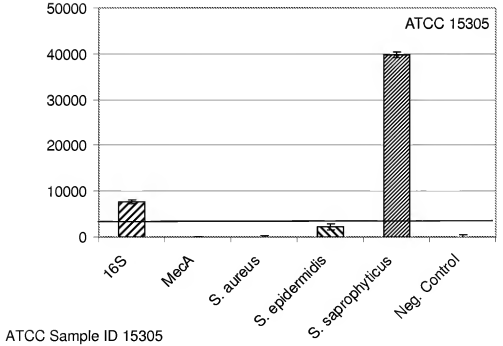
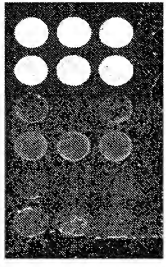


FIG. 19J



ATCC Sample ID 15305

FIG. 20A



ATCC 35984

FIG. 20B

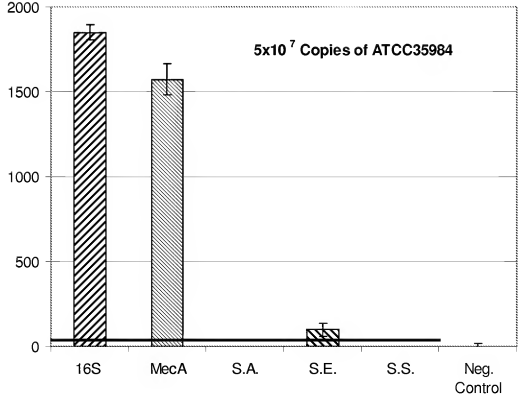
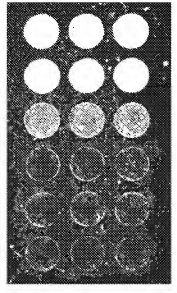


FIG. 20C



ATCC 700699

FIG. 20D

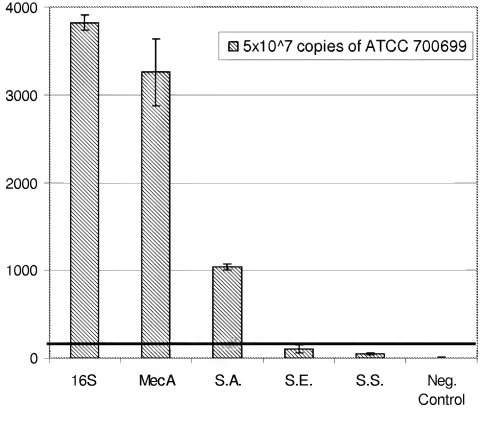
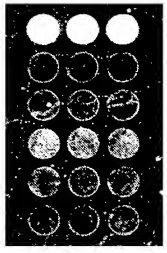


FIG. 20E



ATCC 12228

FIG. 20F

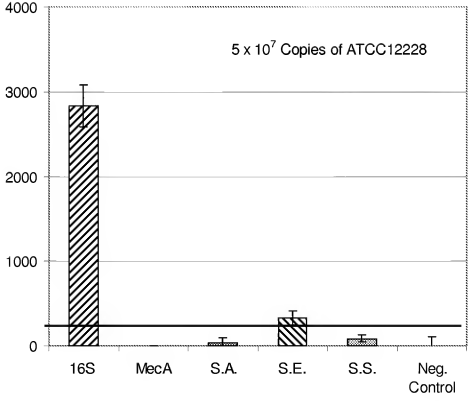
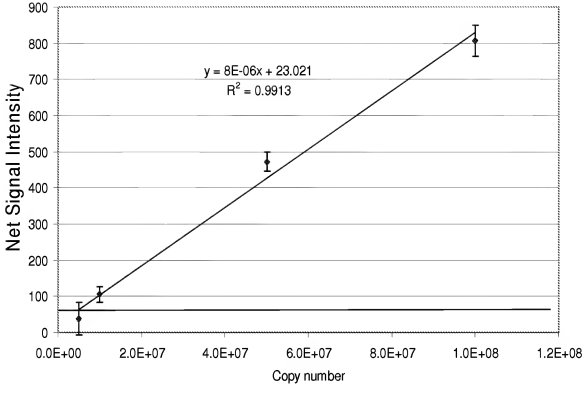


FIG. 21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500
400
300
200
100
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R2 = 0.9913
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2.0E+07
4.0E+07
6.0E+07
8.0E+07
1.0E+08
1.2E+08
Copy number